Computer Science

Data Management Software Development for High-Throughput Proteomics Projects. JEREMY WEATHERFORD (Wheaton College, Wheaton, IL 60187) C.S. GIOMETTI (Argonne National Laboratory, Argonne, IL 60187)

Two-dimensional gel electrophoresis (2DE) is currently the predominant method for the global analysis of proteomes, i.e., the proteins expressed by a biological system. The data output from 2DE proteomics projects is complex, including protein migration coordinates and abundances, protein identifications, and links to genome information. This project involves multiple aspects of the data management requirements of the 2DE proteome projects being conducted by the Argonne National Laboratory's Protein Mapping Group (PMG). The major portion of the work thus far has been in the development of data visualization tools. In addition, tools have been developed to enable multivariate statistical analysis of the 2DE data, automated synchronization of the public genome, proteome and metabolic pathway databases used for identification and interpretation of the 2DE experimental results, and generation of dendrograms at the web server. A project to construct a Linux cluster to expedite multiple-iteration genome sequence searches is currently in progress. The tools developed are being integrated into the data management scheme of PMG.